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SEQUENCE LISTING

<110> HERMANN, Thomas WOLF, Andreas MORBACH, Susanne KRAMER, Reinhard <120> NUCLEOTIDE SEQUENCES CODING FOR THE OtsA PROTEIN <130> 215482US0X <150> DE 10103873.9 <151> 2001-01-30 <150> DE 10110760.9 2000-03-07 <151> <160> 4 <170> PatentIn version 3.1 <210> 1 3010 <211> <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS (884)..(2338) <222> <223> <400> 1 attgcggggc ttactgcgct gatgggttct gcgttttatt acctcttcgt tgtttattta 60 ggccccgtct ctgccgctgc gattgctgca acagcagttg gtttcactgg tggtttgctt 120 gcccgtcgat tcttgattcc accgttgatt gtggcgattg ccggcatcac accaatgctt 180 ccaggtctag caatttaccg cggaatgtac gccaccctga atgatcaaac actcatgggt 240 ttcaccaaca ttgcggttgc tttagccact gcttcatcac ttgccgctgg cgtggttttg 300 ggtgagtgga ttgcccgcag gctacgtcgt ccaccacgct tcaacccata ccgtgcattt 360 accaaggcga atgagttctc cttccaggag gaagctgagc agaatcagcg ccggcagaga 420 aaacgtccaa agactaatca gagattcggt aataaaaggt aaaaatcaac ctgcttaggc 480 gtctttcgct taaatagcgt agaatatcgg gtcgatcgct tttaaacact caggaggatc 540 cttgccggcc aaaatcacgg acactcgtcc caccccagaa tcccttcacg ctgttgaaga 600 ggaaaccgca gccggtgccc gcaggattgt tgccacctat tctaaggact tcttcgacgg

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35 40 45

Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe 50 55 60

Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser 65 70 75 80

Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro 85 90 95

Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp 100 105 110

His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln 115 120 125

Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu 130 135 140

Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly 145 150 155 160

Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu 165 170 175

Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val 180 185 190

Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln 195 200 205

Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu 210 215 220

Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu 225 230 235 240

Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile 245 250 255

Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu 260 265 270

Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg 275 280 285

Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu 290 295 300

Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln 305 310 315

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Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg 340 345 350

Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn 355 360 365

Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro 370 380

Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His 385 390 395 400

Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala 405 410 415

Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser 420 425 430

Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro 435 440 445

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